Claims

1. An AMP deaminase (AMPDA) crystal, wherein said crystal is tetragonal.

2. The crystal of claim 1, wherein said crystal consists essentially of the catalytic domain of AMPDA.

3. The crystal of claim 1, wherein said AMPDA is from a mammal.

4. The crystal of claim 3, wherein the AMPDA is from a rabbit.

5. The crystal of claim 4, wherein the sequence of said AMPDA consists essentially of amino acids 96-747 of SEQ ID NO: 2.

6. The crystal of claim 1, wherein said crystal is grown using citric acid as a precipitating agent.

7. The crystal of claim 1, wherein said crystal is grown in the pH range of 7.80-8.20.

8. The crystal of claim 1, wherein said crystal is grown in the presence of imidazole.

9. The crystal of claim 1, wherein said crystal has a space group $P4_22_12$.

10. The crystal of claim 1, wherein said crystal has unit cell dimensions of a=b=149Å +/- 3Å, c=159Å +/- 3Å.

11. The crystal of claim 1, wherein the active site of said AMPDA is contained in a cleft formed by additional helices between first and second strands of a $(\beta\alpha)_8$ barrel fold, and a helix immediately following a third strand.

12. The crystal of claim 1, wherein said AMPDA has a pocket which can accommodate the adenosine group of AMP, which pocket is formed by amino acid residues including residues His305, Phe372, Phe375, Asp513, Glu575, His594, and Asp650.

13. The crystal of claim 1, wherein said AMPDA has a pocket which can accommodate the ribose and phosphate groups of AMP, which pocket is formed by amino acid residues His305, Ala306, Ala307, Ala308, Phe375, Asn376, Tyr379, Arg388, Lys393, Ser427, Tyr429, Pro460, Ile462, Val512, and Asp513.

14. The crystal of claim 1, wherein said crystal diffracts X-rays to 3.5Å or higher resolution.

15. The crystal of claim 1 further comprising heavy metal atoms.

16. The crystal of claim 1 further comprising an AMPDA inhibitor that has been soaked into said crystal.

17. The crystal of claim 16, wherein said inhibitor is an AMPDA transition state analogue.

18. The crystal of claim 17, wherein said inhibitor is a coformycin analogue.

19. The crystal of claim 18, wherein said inhibitor is coformycin or 3-(2'-(3''-carboxynaphthyl)ethyl)coformycin aglycone.

20. The crystal of claim 1, wherein the primary sequence of said AMPDA has 90% or higher identity at the amino acid level to the sequence shown in SEQ ID NO:2.

21. A method of selecting an AMPDA inhibitor compound from a group of potential AMPDA inhibitor compounds, comprising the following steps:

a) creating a three-dimensional representation of the structure of AMPDA;

b) displaying and superimposing a model of said potential AMPDA inhibitor compound on said representation of the AMPDA structure; and

c) assessing whether said potential AMPDA inhibitor compound model fits said representation of the AMPDA structure.

22. The method of claim 21, further comprising the following steps:

d) incorporating said potential AMPDA inhibitor compound in a biological AMPDA activity assay; and

e) determining whether said potential AMPDA inhibitor compound inhibits AMPDA activity in said assay.

23. A method of selecting an AMPDA inhibitor compound from a group of potential AMPDA inhibitor compounds, comprising the following steps:

a) creating a three-dimensional representation of the active site cavity of AMPDA;

b) displaying and superimposing a model of said potential AMPDA inhibitor compound on said representation of the active site cavity;

c) assessing whether said potential AMPDA inhibitor compound model fits the active site.

24. An isolated and/or purified AMPDA polynucleotide selected from the group consisting of:

a) a polynucleotide encoding the polypeptide as set forth in SEQ ID NO: 2;

b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 1;

c) a polynucleotide comprising a nucleotide sequence that has at least 91% identity to the polynucleotide of any one of (a) or (b);

d) a polynucleotide comprising a nucleotide sequence that has at least 95% identity to the polynucleotide of any one of (a) or (b);

e) a polynucleotide comprising a nucleotide sequence which is capable of hybridising to the polynucleotide of any one of (a) or (b) under high stringency conditions;

f) a complement to the polynucleotide of any one of (a) to (e); and

g) a polynucleotide fragment of the polynucleotide of any one of (a) to (f).

25. An AMPDA polypeptide selected from the group consisting of:

a) a polypeptide having the deduced amino acid sequence translated from the polynucleotide sequence in SEQ ID NO: 1 and variants, fragments, homologues, analogues and derivatives thereof; and

b) a polypeptide of SEQ ID NO: 2 and variants, fragments, homologues, analogues and derivatives thereof.